

ID AC020568 standard; DNA; HTG; 192618 BP.
XX
AC AC020568;
XX
SV AC020568.4 **XP-002192687**
XX
DT 06-JAN-2000 (Rel. 62, Created)
DT 21-JUL-2000 (Rel. 64, Last updated, Version 4)
XX
DE Homo sapiens chromosome 20 clone RP11-206C1, WORKING DRAFT SEQUENCE, 24
DE unordered pieces.
XX
KW HTG; HTGS_DRAFT; HTGS_PHASE1.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-192618
RA Waterston R.H.;
RT "The sequence of Homo sapiens clone";
RL Unpublished.
XX
RN [2]
RP 1-192618
RA Waterston R.H.;
RT ;
RL Submitted (04-JAN-2000) to the EMBL/GenBank/DDBJ databases.
RL Genome Sequencing Center, Washington University School of Medicine, 4444
RL Forest Park Parkway, St. Louis, MO 63108, USA
XX
CC On Jul 19, 2000 this sequence version replaced gi:9211362.
CC ----- Genome Center -----
CC Center: Washington University Genome Sequencing Center
CC Center code: WUGSC
CC Web site: <http://genome.wustl.edu/gsc/index.shtml>
CC ----- Project Information -----
CC Center project name: H_NH0206C01
CC ----- Summary Statistics -----
CC Sequencing vector: M13; 93%
CC Sequencing vector: plasmid; 7%
CC Chemistry: Dye-primer ET; 93% of reads
CC Chemistry: Dye-terminator Big Dye; 7% of reads
CC Assembly program: Phrap; version 0.990319
CC Consensus quality: 179082 bases at least Q40
CC Consensus quality: 183120 bases at least Q30
CC Consensus quality: 185448 bases at least Q20
CC Insert size: 205000; agarose-fp
CC Insert size: 190318; sum-of-contigs
CC Quality coverage: 3.99 in Q20 bases; agarose-fp
CC Quality coverage: 4.34 in Q20 bases; sum-of-contigs
CC -----
CC * NOTE: This is a 'working draft' sequence. It currently
CC * consists of 24 contigs. The true order of the pieces
CC * is not known and their order in this sequence record is
CC * arbitrary. Gaps between the contigs are represented as
CC * runs of N, but the exact sizes of the gaps are unknown.
CC * This record will be updated with the finished sequence
CC * as soon as it is available and the accession number will
CC * be preserved.
CC *
CC * 1 1279: contig of 1279 bp in length
CC * 1280 1379: gap of unknown length
CC * 1380 3544: contig of 2165 bp in length
CC * 3545 3644: gap of unknown length
CC * 3645 5441: contig of 1797 bp in length
CC * 5442 5541: gap of unknown length
CC * 5542 8421: contig of 2880 bp in length
CC * 8422 8521: gap of unknown length
CC * 8522 10096: contig of 1575 bp in length
CC * 10097 10196: gap of unknown length
CC * 10197 11938: contig of 1742 bp in length

P.D. 06-01-2000	5
p. 1-5 =	

CC	*	11939	12038: gap of unknown length
CC	*	12039	14708: contig of 2670 bp in length
CC	*	14709	14808: gap of unknown length
CC	*	14809	17876: contig of 3068 bp in length
CC	*	17877	17976: gap of unknown length
CC	*	17977	21534: contig of 3558 bp in length
CC	*	21535	21634: gap of unknown length
CC	*	21635	24615: contig of 2981 bp in length
CC	*	24616	24715: gap of unknown length
CC	*	24716	28301: contig of 3586 bp in length
CC	*	28302	28401: gap of unknown length
CC	*	28402	35969: contig of 7568 bp in length
CC	*	35970	36069: gap of unknown length
CC	*	36070	42473: contig of 6404 bp in length
CC	*	42474	42573: gap of unknown length
CC	*	42574	49752: contig of 7179 bp in length
CC	*	49753	49852: gap of unknown length
CC	*	49853	57604: contig of 7752 bp in length
CC	*	57605	57704: gap of unknown length
CC	*	57705	67088: contig of 9384 bp in length
CC	*	67089	67188: gap of unknown length
CC	*	67189	77656: contig of 10468 bp in length
CC	*	77657	77756: gap of unknown length
CC	*	77757	92143: contig of 14387 bp in length
CC	*	92144	92243: gap of unknown length
CC	*	92244	109240: contig of 16997 bp in length
CC	*	109241	109340: gap of unknown length
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CC	*	138709	153882: contig of 15174 bp in length
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CC	*	153983	169994: contig of 16012 bp in length
CC	*	169995	170094: gap of unknown length
CC	*	170095	192618: contig of 22524 bp in length.

XX

FH	Key	Location/Qualifiers
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FT	misc_feature	5542..8421
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FT	misc_feature	8522..10096
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FT	misc_feature	10197..11938
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FT		/note="assembly_name:Contig26"
FT	misc_feature	14809..17876
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Sequence 192618 BP; 56353 A; 40444 C; 39339 G; 54167 T; 2315 other;

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